

DBT/ Centre for DNA Fingerprinting and Diagnostics (CDFD), Hyderabad

CDFD scientists conduct global secretome characterization of the pathogenic yeast *Candida glabrata*

By Sunderarajan Padmanabhan

New Delhi, February 24: *Candida glabrata* is an opportunistic human fungal pathogen, which is a common cause of hospital-acquired bloodstream infections. There is a need to uncover the mechanisms that helps it to establish successful and life-threatening infections in humans. Towards this end, scientists at Centre for DNA Fingerprinting and Diagnostics (CDFD), Hyderabad, had previously shown that a family of 11 cell surface-associated aspartyl proteases is required for the pathogenesis of *C. glabrata* in a mouse model of *C. glabrata*-caused human disease. These proteases are crucial factors, as these help *C. glabrata* survive different kinds of stresses and maintain the cell surface in a manner that keeps activation of the host immune system in check.

In the current study, the scientists have shown that the 11 cell surface aspartyl proteases also regulate the number and the kind of proteins that are secreted out into the environment during regular growth. We show that the *C. glabrata* cells lacking proteases secrete out 4.6-fold higher number of proteins, compared to the cells that contain these proteases. We further show the divergent nature of secretory proteins of *C. glabrata* cells lacking aspartyl proteases.

These results are of high importance, as human pathogens frequently evade the host immune response by altering the nature and the properties of the proteins, they secrete, upon exposure/contact with the host. In short, the current work has advanced our understanding of the pathobiology of an important human pathogen *C. glabrata*, and may lead to the development of better intervention strategies to control *Candida* infections.

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